

Figures

Figure 1 - Nucleotide and protein sequence of *Aspergillus ochraceus* 11 alpha hydroxylase

5	tggaagtttt tacacttatt atgcgggagc cgaagatttc tgagtcgagg ggttggggaa	60
	caactatata agacctacaa ccacttggat ttgttgaatt tacacgggca ttatcaaaac	120
	agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg	172
	Met Pro Phe Phe Thr Gly Leu Leu Ala	
10	att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc	220
	Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr	
15	att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc	268
	Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser	
20	gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt	316
	Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg	
25	cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg	364
	Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg	
30	ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg	412
	Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp	
35	gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac	460
	Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn	
40	gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga	508
	Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly	
45	tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa	556
	Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys	
50	gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg	604
	Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro	
55	atc tgc cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat	652
	Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp	
60	cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc	700
	Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val	
65	gcc cgg atg tgc aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac	748
	Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn	
70	cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt	796
	Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly	
75	gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta	844
	Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val	
80	cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tgc ctg cga cgc	892
	His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg	
85	tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag	940
	Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys	
90	ggg acc acg gac gag cag gcc aag ccc ctt atg ttt gat gat tcc atc	988
	Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile	

	gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys 285 290 295	1036
5	cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu 300 305 310	1084
10	tgg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala 315 320 325	1132
15	gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys 330 335 340 345	1180
20	gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser 350 355 360	1228
25	cag cgt ctc agg cct acg ctt ctc gcc tcc ttt cgt cgg cag gca acg Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Gln Ala Thr 365 370 375	1276
30	aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg 380 385 390	1324
35	gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp 395 400 405	1372
40	cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro 410 415 420	1420
45	ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met 430 435 440	1468
50	gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser 445 450 455	1516
55	aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp 460 465 470	1564
60	cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr 475 480 485	1612
65	tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala 490 495 500 505	1660
	gag atc gat atg gcg agt tta act gtg tag gtgcaaacag aagtcctgat Glu Ile Asp Met Ala Ser Leu Thr Val *	1710
	gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtacaat ttataagaat aaaaaa	1770 1776

**Figure 2 - Nucleotide and protein sequence of human
oxidoreductase**

5	atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val 1 5 10 15	48
10	gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser 20 25 30	96
15	ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag asa aaa Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys 35 40 45	144
20	gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val 50 55 60	192
25	aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile 65 70 75 80	240
30	atc gtg ttc tac gcc tcc cag acg ggg act gca gag gag ttt gcc aac Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Phe Ala Asn 85 90 95	288
35	cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga gcc atg tca cgc Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala 100 105 110	336
40	gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile 115 120 125	384
45	gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp 130 135 140	432
50	ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp 145 150 155 160	480
55	gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys 165 170 175	528
60	acc tac gag cac ttc aat gcc atg gcc aag tac gtg gac aag cgg ctg Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu 180 185 190	576
65	gag cag ctc gcc gcc cag cgc atc ttt gag ctg ggg ttg gcc gac gac Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asn 195 200 205	624
70	gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp 210 215 220	672
75	cgc gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act gcc gag gag tcc Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser 225 230 235 240	720
80	agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala 245 250 255	768
85	aag gtg tac atg ggg gag atg gcc cgg ctg aag agc tac gag aac cag Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Glu Ser 260 265 270	816
90	aag ccc ccc ttt gat gcc aag aat cgg ttc ctg gct gca gtc acc acc Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr 275 280 285	864
95	aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu 290 295 300	912
100	ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtc Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val 305 310 315	960

10021425 100004

	305	310	315	320	
5	gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg gcc aaa Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys 325 330 335	1008			
	atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Leu Asp 340 345 350	1056			
10	gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg 355 360 365	1104			
15	acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn 370 375 380	1152			
20	gtg ctg tac gag ctg gcg cag tac gcc tgg gag ccc tgg gag cag gag Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu 385 390 400	1200			
25	ctg ctg cgc aag atg gcc tcc tcc tcc ggc gag ggc aag gag ctg tac Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr 405 410 415	1248			
	ctg agc tgg gtg gtg gag gcc cgg agg cac atc ctg gcc atc ctg cag Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln 420 425 430	1296			
30	gac tgc ccg tcc ctg ccg ccc ccc atc gac cac ctg tgt gag ctg ctg Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu 435 440 445	1344			
35	ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val 450 455 460	1392			
40	cac ccc aac tct gtg cac atc tgt ccg gtg gtt gtg gag tac gag acc His Pro Asn Ser Val His Ile Cys Ala Val Val Glu Gly Tyr Glu Thr 465 470 475	1440			
45	aag gcc gcc cgc atc aac aag gcc gtg gcc acc aac tgg ctg ccg gcc Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala 485 490 495	1488			
50	aag gag cct gcc ggg gag aac gcc gcc cgt ccg ctg gtg ccc atg ttc Lys Glu Pro Ala Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe 500 505 510	1536			
55	gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc aag cct gtc Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val 515 520 525	1584			
	atc atg gtg gcc ccc gcc acc ggg gtg gca ccc ttc ata gcc ttc atc Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile 530 535 540	1632			
60	cag gag ccg gcc tgg ctg cga cag cag gcc aag gag gtg ggg gag acg Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr 545 550 555 560	1680			
65	ctg ctg tac tac gcc tgc cgc cgc tgg gat gag gac tac ctg tac ccg Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg 565 570 575	1728			
70	gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn 580 585 590	1776			
	gtg gcc ttc tcc ccg gag cag tcc cac aag gtc tac gtc cag cac ctg Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu 595 600 605	1824			
75	cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa gcc ggt gcc Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala 610 615 620	1872			
80	cac atc tac gtc tgt ggg gat gca cgg aac atg gcc agg gat gtg cag His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln 625 630 635 640	1920			
85	aac acc ttc tac gac atc gtg gct gag ctc ggg gcc atg gag cac gcg Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala 645 650 655	1968			

10021425-103004

	cag gcg gtg gac tac atc aag aaa ctg atg acc aag ggc cgc tac tcc	2016
	Gln Ala Val Asp Tyr Ile Lys Lys Leu Met Thr Lys Gly Arg Tyr Ser	
	660	
	665	
	670	
5	ctg gac gtg tgg agc	2031
	Leu Asp Val Trp Ser	
	675	

10024425.103001

Figure 3 - Nucleotide and protein sequence of *Aspergillus ochraceus* oxidoreductase

5	cttatttcgt ttaggaaagag caccggcttc ggtgtccttc cttaccctct tattcttctc ctctgactc cctttttgtt attgategcc catctgggtg aacatttggg atactcttcc ctctcccctt cccgcccoga cctctcttat ctctctctcc cgtccagcat ttagctcgcc atcgaaatcg caattctctc ctctgtgact tcatcgtgtg agcgtectca tc atg ggc Met Ala 1	60 120 180 238
10	caa ctc gat act ctc gat ttg gtc gtc cts gts ggc ctc ttg gts ggt Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly 5 10 15	286
15	agc gtc ggc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp 20 25 30	334
20	cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly 35 40 45 50	382
25	aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys 55 60 65	430
30	gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser 70 75 80	478
35	aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gts Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val 85 90 95	526
40	gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu 100 105 110	574
45	gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Gly Glu Gly Pro 115 120 125 130	622
50	acg gat aat gcg gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala 135 140 145	670
55	gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu 150 155 160	718
60	aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn 165 170 175	766
65	gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln 180 185 190	814
70	cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu 195 200 205 210	862
75	gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu 215 220 225	910
80	gcy att aac ctg caa gag cgc gat gcy gtc tac gag ccg gtc ttc aat Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn 230 235 240	958
85	gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu 245 250 255	1006
90	ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr 260 265 270	1054
95	tct gcy cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu 275 280 285 290	1102

1002425-100004

	ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala 295 300 305	1150
5	ggt agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro 310 315 320	1198
10	acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu 325 330 335	1246
15	gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr 340 345 350	1294
20	gct aag gtt cgg att ccc act cct acg acc tat gac gcc gca gtt cgc Ala Lys Val Pro Ile Pro Thr Pro Thr Thr Tyr Asp Ala Ala Val Arg 355 360 365 370	1342
25	tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tgc act Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr 375 380 385	1390
30	ctc gct gcc ttt gcc cct gat gaa cgc acc aag cgc gag atc gtt cgt Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg 390 395 400	1438
35	ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys 405 410 415	1486
40	ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr 420 425 430	1534
45	gcc gtc cgg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro 435 440 445	1582
50	cgt tac tac tgg atc tcc tgg tct tcc ctg gtt cag aag gac aag att Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile 455 460 465	1630
55	agc att acc gcc gtt gtg gag tgg gtt cgc ttg cct ggt gag gaa cac Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His 470 475 480	1678
60	att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys 485 490 495	1726
65	caa aac gcg gag cct tcc cct gac cgc cac gcc ttg act tac tct atc Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile 500 505 510	1774
70	act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val 515 520 525 530	1822
75	cgc cac tgg aac ttc aaa ttg ccc tgg gat ccc tgg cga cct gtg atc Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile 535 540 545	1870
80	atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln 550 555 560	1918
85	gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu 565 570 575	1966
90	ctt ttc ttc gcc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp 580 585 590	2014
95	gaa tgg aag act ttt cag gag cag ctt gcc gac tgc ctc aag atc atc Glu Tyr Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile 595 600 605 610	2062
100	act gcc ttc tct cgt gaa tgg gct gag aaa gtc tac gtc cag cac agg Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg 615 620 625	2110
105	ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag aaa gcc	2158

1002425-10004

	Leu Arg Glu His Ala Glu Leu Val Ser Asp Leu Leu Lys Gln Lys Ala 630 635 640	
5	act ttc tat gtt tgc ggt gac gct gcc aac atg gcc cgt gaa gtc aac Thr Phe Tyr Val Cys Gly Asp Ala Ala Asn Met Ala Arg Glu Val Asn 645 650 655	2206
10	ctc gtg ctt ggg caa atc att gcc aag cag cgc ggt ctc cct gcc gag Leu Val Leu Gly Gln Ile Ile Ala Lys Gln Arg Gly Leu Pro Ala Glu 660 665 670	2254
15	aag ggc gag gag atg gtg aag cac atg cgc agc agc ggc agc tac cag Lys Gly Glu Glu Met Val Lys His Met Arg Ser Ser Gly Ser Tyr Gln 675 680 685 690	2302
	gac gat gtc tgg tcc taa aa Asp Asp Val Trp Ser * 695	2322

10021425.103001

Figure 4 - Amino acid homology alignment of *A. ochraceus* 11 alpha hydroxylase with the top 10 BLAST hits from GenBank

CAA75565	1	---MANHSSSYHYEFYKDHSTVL	LMSEKPVILPSL	ILGTCAVLICIQWLK	---PQPLIM
CAB91316	1	-----MERLDIKSI	DPSPATFP	SYLVTAFLAVV	SIQGPFP--PKNTKH
CAB56503	1	-----LLFCF	ILSKTTKK	GGNSQYS	---NHDELPL
AAB94588	1	-----MVVEL	LNHNTPF	LYPTITSL	IFPVPFKLVORS---DSKTS--STCKPL
pMON45624	1	-----HFF	LPFLAVQVTL	STVFLAAAL	---LATLQ---RSDLPL
CAA75566	1	-----MSIFNMITSYAGS	QLLPFYIA	IFPVLVP	WALTR--SWLELRK--GSVPL
AAD34552	1	---MTVDALTQPHHLS	LAWNDTQ	QHGSGW	FAPLVTTSAGLLCLLL--LSCSGR---RSDLPLV
CAA75567	1	-----			
CAA76703	1	MSKSN	SNMSTSHETLF	QQLVLGLDRMP	MDVHMLTVAFGAWLCS
CAA57874	1	-----			
CAA91268	1	-----MALLTL	SLVSI	ITFFIYII	LAARREK
					KLREKTLGSGPEPH
CAA75565	56	VNRK	FGELSNV	ARCTF	FGCAQ
CAB91316	45	LA	IKPFLSDT	---FKK	IVYGS---
CAB56503	20	PG	PTPLPLGNA	QLSGH	---TH
AAB94588	45	PG	RTLPLIGNI	QIVGSL	LVHYIY
pMON45624	46	LN	AKPFETNR	RVHE	VENS
CAA75566	48	AN	TPD	SLFGTG	---
AAD34552	56	PK	QWEL	TL	---
CAA75567	1	-----			
CAA76703	61	VVG	RSVFETWLL	SLR	FWEGGS
CAA57874	1	-----			
CAA91268	43	WFLGN	LKQTAER	---	---

CAA75565	116	NEK	---	---	---
CAB91316	105	DDR	---	---	---
CAB56503	86	THD	---	---	---
AAB94588	104	THD	---	---	---
pMON45624	106	DR	---	---	---
CAA75566	107	DR	---	---	---
AAD34552	115	MKE	---	---	---
CAA75567	1	-----			
CAA76703	121	LS	---	---	---
CAA57874	1	-----			
CAA91268	102	KNFS	---	---	---

CAA75565	170	E	---	---	---
CAB91316	159	Q	---	---	---
CAB56503	146	E	---	---	---
AAB94588	163	E	---	---	---
pMON45624	156	H	---	---	---
CAA75566	161	R	---	---	---
AAD34552	169	N	---	---	---
CAA75567	17	M	---	---	---
CAA76703	173	E	---	---	---
CAA57874	1	-----			
CAA91268	159	SKVD	---	---	---

CAA75565	227	V	---	---	---
CAB91316	218	D	---	---	---
CAB56503	202	A	---	---	---
AAB94588	213	A	---	---	---
pMON45624	213	A	---	---	---
CAA75566	218	T	---	---	---
AAD34552	226	V	---	---	---
CAA75567	70	Q	---	---	---
CAA76703	232	E	---	---	---
CAA57874	1	-----			
CAA91268	217	E	---	---	---

10021425.100001

CA75565 283 ERTGKRV-TYNDARELDLDLAREK---SVGYDPACAGSELSAR---HHTDPFTQVVEF
 CAB91316 274 ---SKA-EHDAEAPERTA-K---SKYYPAAAVVSVVA---HHTEDLTCTCVPMI
 CAB56503 259 G-EKKP-DLVTPAATQRADPE---PLASKNKQVPLVPSVSGTTSPTTQWCSW
 AAB94588 276 R-EAVE-DLVTPALKFQRES---E-FLTDNKKAKIOTDPIGGGESSVSWMCSW
 pMON45624 269 DECKPL-MPDSERFEREL-----SPNDAVKKQLSLVS---HHTSDLLQWNSL
 CA75566 274 IAAQPLPVFHDAEDSEQEAAAGTASFPVPEFQVQSLAS---HHTVDLQOOTMDI
 AAD34552 282 KAKTEPHRYVVSQFEDTAK---SKWLAAGAAADAFAS---VQISDLTIGLVDI
 CA75567 129 TLLDYTEGRGTSCALRHLP-RELAFTQVQVGGDQIETFA---HSTVAFTVSLI
 CA76703 282 ---SGN---ELTSSKNDATGEE-KQIDIAORMVLSIAS---HHTMTHTVWMDL
 CA57874 44 ---LEDPTMLDHLNGRNEHIA---DDVBLQHPHSLIAVE---TVVTSSTQSTVDI
 CA91268 277 RRRGEGSDSVTLKLLNREDDKS-KPMTKQELTNCFFLLAGVSTSTATVTCYSYL

CA75565 338 AONPELEPREEINAKGKC---KRSSTAYMLGLDSVVKESRR
 CAB91316 324 ONPPEADLPPEETIOASEG---KRSSTAYMLGLDSVVKESRR
 CAB56503 314 KAPTEPKKACQVVRKNEKN---VDETHKQVRLQVVKEDH
 AAB94588 329 EAPGPEEADQSRVDSKGE---VDETHKQVRLQVVKEDH
 pMON45624 321 AONKQLEAAREVVRSTES---LSASVSLDGLDQAKESRR
 CA75566 332 GHPPELEPREEVVOREE---KPTTFKMLGLDQAKESRR
 AAD34552 336 TPPEPEELRLRRTIQGCG---TPPASVYKMLDQAKESRR
 CA75567 186 LKPEPEELRLRRTIQGCGVSPDICINSSKRLDSDFEHRRC
 CA76703 333 CAPEPELEPREEVVRSTES---LTPVPLDGLDQAKESRR
 CA57874 96 LKPEPELEPREEVVRPRDNGN---TPDSIVAMKLDQAKESRRNSGLMSNL
 CA91268 336 SEVPEVCEPREEVMEAKNGE---LTVTSVHMYDQVVKELRIFY

CA75565 384 -----IAIASRPHPTTHRSGVILPINKLTIKSAIHW-----DGVTKE
 CAB91316 370 -----TGVAIRYAEKQLSLSGTTPKSGVMAASADW-----NSBVRG
 CAB56503 361 -----PVPLLTPRCREQCRKLTPTTISKVGLDQANAGR-----DNYTIE
 AAB94588 376 -----PVPLLTPVERERCCN-STPTSKVGLDQANAGR-----NXYIGE
 pMON45624 367 -----TLLECPRQATNCKSGSKVGTQVGLDQANAGR-----NDYVIE
 CA75566 378 -----GSIVHREYVTEPLSLSLTKGTITNNNRD-----DKTINP
 AAD34552 382 -----VECAQSEYALQDTSNGTTPKGLADADRIS-----NPEVME
 CA75567 238 -----STFVPSRMVMSKSLNTRKLTGTAFATPAHMSSETPTSTPSS
 CA76703 379 -----VPLLEPAVLYKSGPLSGTSTSTPTTDEALO-----DSARVG
 CA57874 152 KNYKLCESLTHSNPTITIAKLPDTPPKGTQDNTCSHK-----DHKLIN
 CA91268 382 -----PHFSFRRLCREDTIR-LQPYPKGATVCLPTDHR-----NENMDS

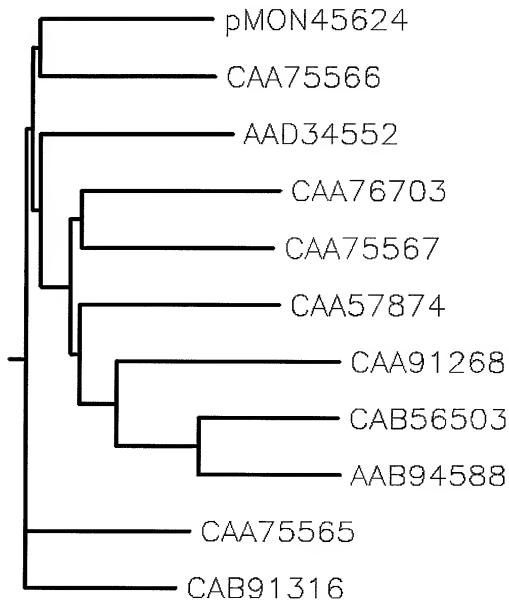
CA75565 427 LKK-----DGRPEFNNREP---SKSKAQLVATPTNPFVLIACPRFPFASERK
 CAB91316 413 LKK-----DGRPEFLRBTTPGAKENNAQLVAPHPGPHGACPRFPFANEK
 CAB56503 404 LKK-----DGRPEFLS-----VDFKQNSFVFPVGGGRITDPTTIPALANIK
 AAB94588 419 LKS-----DGRPEFLNS-----S-IDFKQDFPEFPCARSLTPITPHIPSLIK
 pMON45624 410 LQO-----DGRPEFNVYFP---EDKMLALGSAHNVGPHGACPRFPFASNEIK
 CA75566 421 LEV-----DGRPEFLDSEEA-SGDHGAQLVSGSNHVPFHGACPRFPFANEIK
 AAD34552 425 LAK-----DGRPMRREDP---RAPSQALENGHHPGPHGACPRFPFASKETIK
 CA75567 289 LNPSPRTDGLRLNLSIK---EGSGSHAAALGPEYITDHPHACPRFPFASIK
 CA76703 423 LTP-PTEDGKSKSDS---NAYAKLFPDSSVHTDHPHACPRFPFASNEIK
 CA57874 205 LEO-----DGRPEFLKWKAP---SEKKRYSSGTQDSSAKRPHACPRFLAINIK
 CA91268 425 LEE-----DHPREPRNWE-----E---RSSEKIKVPEVPEFTVQVPRFAMPEFT

CA75565 480 AEGHLLNLTDFV-----EGSSMEPRKYDANANPALESLPRKREAI
 CAB91316 468 AVHLLNLTDFV-----EGSDPKRTTFESGVTSGLLEYGQPEHEL
 CAB56503 449 PAQLPLPDQSS-----NTEKLNKKE-SRPTREDLDLTPVNFSSSSPA
 AAB94588 464 PAACLPLPDQSSNGMNEELMTE-SNPTREDLDLTPITP-----TP
 pMON45624 463 ALCHLLNLTDFV-----DQKPOLNLTATVLALETPR-ARDMASV
 CA75566 474 ALCHLLNLTDFV-----PDTEKPTDTRNANSSVTDLLNRESSEVLEAL
 AAD34552 478 MEAYLLNLTDFV-----PDEPLQYRHFSRIHETPRGRD-EDRLPLGSL
 CA75567 347 LITELANDME-----DGKPGPELMRVETITLDTKAGLDRSR
 CA76703 479 LITELANDME-----DGKRPNTIDSPVETITLDTKAGLDRSRDE
 CA57874 258 LITELANDME-----DGLSRFKIEFELASIAACANA
 CA91268 468 TEVKLPTDTEKDF-----EGEADLPDCNLTTPNDPVLNLSGN

85 CA75565 (SEQ ID NO: 27)
 CAB91316 (SEQ ID NO: 28)
 CAB56503 (SEQ ID NO: 29)
 AAB94588 (SEQ ID NO: 30)
 pMON45624 (SEQ ID NO: 02)
 CA75566 (SEQ ID NO: 31)
 AAD34552 (SEQ ID NO: 32)
 CA75567 (SEQ ID NO: 33)
 CA76703 (SEQ ID NO: 34)
 CA57874 (SEQ ID NO: 35)
 CA91268 (SEQ ID NO: 36)

1004126.10001

Figure 5 - Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* 11 alpha hydroxylase to the top 10 BLAST hits from GenBank



**Figure 6 – Percent homology of *Aspergillus ochraceus* 11
alpha hydroxylase to the top 10 BLAST hits from GenBank**

Accession Number	Species	% ID to 11a OH
CAB91316	<i>Neurospora crassa</i>	40
CAA76565	<i>Gibberella fujikuroi</i>	37
CAA75566	<i>Gibberella fujikuroi</i>	37
AAD34552	<i>Aspergillus terreus</i>	29
CAA75567	<i>Gibberella fujikuroi</i>	24
CAA57874	<i>Fusarium oxysporum</i>	24
CAA76703	<i>Gibberella fujikuroi</i>	23
CAB56503	<i>Catharanthus roseus</i>	14
AAB94588	<i>Glycine max</i>	14
CAA91268	<i>Caenorhabditis elegans</i>	12

10021425:103001

Figure 7 – Amino acid homology alignment of *A. ochraceus* and human oxidoreductase to NADPH cytochrome P450 reductases from *A. niger*, mouse, and *S. cerevisiae*

5	PMON45605	1	MGDSHVTSTQVSPVAVVEVSLSTEDMLLSLIVGLAVYVPLFKKKKEPPEFSKIQTL	
	human	1	MGDSHVTSTQVSPVAVVEVSLSTEDMLLSLIVGLAVYVPLFKKKKEPPEFSKIQTL	
	mouse	1	MGDSHVTSTQVSPVAVVEVSLSTEDMLLSLIVGLAVYVPLFKKKKEPPEFSKIQTL	
	PMON45632	1	--MGDLDLDDLVLLVALLVGSVAYFKG-----YYAARDPYA--SAGPAVGG	
10	niger	1	--MGDLDLDDLVLLVALLVGSVAYFKG-----YYAARDPYA--LPAPVWGA	
	yeast	1	--MPFGDLDLDDLVLLVALLVGLVKKRN-----SIKPLMSDDG-----DT--	
15	PMON45605	61	TSSVLSSEVEKVKIKGTQNLIVFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
	human	61	TSSVLSSEVEKVKIKGTQNLIVFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
	mouse	61	TPPVLSSEVEKVKIKGTQNLIVFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
	PMON45632	47	AKGCTGRDITDKNDENY--G--GPFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
20	niger	47	AKGCTGRDITDKNDENY--G--GPFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
	yeast	42	ES--GCONRDIA--ITENALVY--G--GPFYGSQTGTAFTHANKLSKTHRRVONRQMSADPBEYDL	
25	PMON45605	120	ADLSLPEITDNLAVFCMATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
	human	120	ADLSLPEITDNLAVFCMATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
	mouse	120	ADLSLPEITDNLAVFCMATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
	PMON45632	107	EULEKPLD--DK--AFVLYATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
30	niger	107	EULEKPLD--DK--AFVLYATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
	yeast	102	ES--NDMLFV-----NSIFPLATYGEQDPTDNLADFYDMLG-----SI-----DVDLSGMRK	
35	PMON45605	169	AVFGLGNITYEHFNAMGKYVDKRLDGLGQRIPLALDSD--DNLSEEDPTDPEQVPAV	
	human	169	AVFGLGNITYEHFNAMGKYVDKRLDGLGQRIPLALDSD--DNLSEEDPTDPEQVPAV	
	mouse	169	AVFGLGNITYEHFNAMGKYVDKRLDGLGQRIPLALDSD--DNLSEEDPTDPEQVPAV	
	PMON45632	165	VTFGLGNITYEHFNAMVVDALDKFQADRIQSAGSGDDGAGTDEEDFA--KPPPMAL	
40	niger	164	VAFGLGNITYEHFNAMVVDALDKFQADRIQSAGSGDDGAGTDEEDFA--KPPPMAL	
	yeast	148	NFGLGNITYEHFNAMVVDALDKFQADRIQSAGSGDDGAGTDEEDFA--KPPPMAL	
45	PMON45605	228	CBFGVATGGESSITROYLVTHD-----DAAVYVGEGRSLIS-----ENQKP	
	human	228	CBFGVATGGESSITROYLVTHD-----DAAVYVGEGRSLIS-----ENQKP	
	mouse	228	CBFGVATGGESSITROYLVTHD-----DAAVYVGEGRSLIS-----ENQKP	
	PMON45632	225	SAMNLT--LRDAVYVFNVDDESISPDENVYLGHPYQGLQ-----GEFG	
50	niger	224	SSMDLT--LRDAVYVFNVDDESISPDENVYLGHPYQGLQ-----GEFG	
	yeast	208	KDELH-----SEAKFTSPQPTVLN-----ETDSSGFSHLYPSQLINRNADNLGL	
55	PMON45605	275	PFDAKNPFPAATNRRKNGGTTHHMLELDTDSRLRYEGDHWAVVPANDSALVNL	
	human	275	PFDAKNPFPAATNRRKNGGTTHHMLELDTDSRLRYEGDHWAVVPANDSALVNL	
	mouse	275	PFDAKNPFPAATNRRKNGGTTHHMLELDTDSRLRYEGDHWAVVPANDSALVNL	
	PMON45632	273	PFSANPFPAPAESSEPFVQNGCHLESLDSESLDGLDHWAVVPANDSALVNL	
60	niger	272	PFSANPFPAPAESSEPFVQNGCHLESLDSESLDGLDHWAVVPANDSALVNL	
	yeast	262	PFLSPPFPAPVKSSEPFSSNINCHLESLDSESLDGLDHWAVVPANDSALVNL	
65	PMON45605	335	GKLLQAL--LVVMSINLDEESSKHPFFCPPTTYRPLALYYLITNPPTLVLYELAQ	
	human	335	GKLLQAL--LVVMSINLDEESSKHPFFCPPTTYRPLALYYLITNPPTLVLYELAQ	
	mouse	335	GKLLQAL--LVVMSINLDEESSKHPFFCPPTTYRPLALYYLITNPPTLVLYELAQ	
	PMON45632	333	LQAFGLGKRHSVNNKGE--VITAVIITPTTYDANRYVLYCAVSRVFTSLTAS	
70	niger	332	LQAFGLGKRHSVNNKGE--VITAVIITPTTYDANRYVLYCAVSRVFTSLTAS	
	yeast	322	LSLENLG--FETPLDKFL--PTVAVFPTPTTIGARPLRLT--EVSRIQPSSTLTG	
75	PMON45605	393	AG--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
	human	393	AG--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
	mouse	393	AG--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
	PMON45632	391	AP--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
80	niger	390	AP--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
	yeast	378	AP--PSPQQLLRKMASSSGSGKELYLSVVVEARRHILALLOIC--SLRPPIDHLCPLLP	
85	PMON45605	451	LAARYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	
	human	451	LAARYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	
	mouse	451	LAARYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	
	PMON45632	448	LCPYYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	
90	niger	446	LCPYYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	
	yeast	436	LCPYYYSASSSSVFNNSVITCAVAVETIK-----AGRINKQAVNWLRAKEF--AGE--	

10021425.103001

2013

Figure 8 – Amino acid homology alignment of *A. ochraceus* oxidoreductase to NADPH cytochrome P450 reductases from *A. niger* and *S. cerevisiae*

5	<i>A. niger</i>	1	-NAQIDTLDDLWVLLVGLVGSVAYFPKGTYYAAVAKRMPPLPFRMCKRAGKGTITITRGR
	<i>A. ochraceus</i>	1	-NAQIDTLDDLWVLLVGLVGSVAYFPKGTYYAAVAKRMPPLPFRMCKRAGKGTITITRGR
	<i>S. cerevisiae</i>	1	MPFGVNDLPTVLAHLVGLVGLVGRNLIKELMDDDDITAVSS-----NRDIAV
	<i>A. niger</i>	60	EECKGVVTFPGSGGTAEQVSRIAKGGSORPGLKTVADLELYOVNATGPEPKVYV
	<i>A. ochraceus</i>	60	EECKGVVTFPGSGGTAEQVSRIAKGGSORPGLKTVADLELYOVNATGPEPKVYV
10	<i>S. cerevisiae</i>	55	TENNNTVTVLVSCTGTAEQVSRIAKGGSORPGLKTVADLELYOVNATGPEPKVYV
	<i>A. niger</i>	120	FVLTATVGGEGPTDNAVETQPTGCEVAFESAAATKPLSKKYVAFGLGNTVYEHYA
	<i>A. ochraceus</i>	120	FVLTATVGGEGPTDNAVETQPTGCEVAFESAAATKPLSKKYVAFGLGNTVYEHYA
	<i>S. cerevisiae</i>	113	IPSTVYGGEGPTDNAVETQPTGCEVAFESAAATKPLSKKYVAFGLGNTVYEHYA
15	<i>A. niger</i>	179	AVRVYDAVFCRLRPORTGSAGSGDDGACTMEEDFLAWKPPMHAALSESMLEREAVYER
	<i>A. ochraceus</i>	180	AVRVYDAVFCRLRPORTGSAGSGDDGACTMEEDFLAWKPPMHAALSESMLEREAVYER
	<i>S. cerevisiae</i>	163	AAVKAQVFCRLRPORTGSAGSGDDGACTMEEDFLAWKPPMHAALSESMLEREAVYER
20	<i>A. niger</i>	239	VEQVTEENSLSPLELVYLGEPTQSHIA-----TPKGPYSAHNPPIAPISRESRL
	<i>A. ochraceus</i>	240	VEQVTEENSLSPLELVYLGEPTQSHIA-----TPKGPYSAHNPPIAPISRESRL
	<i>S. cerevisiae</i>	223	QEQVTEENSLSPLELVYLGEPTQSHIA-----TPKGPYSAHNPPIAPISRESRL
25	<i>A. niger</i>	290	FWVKDRNCLHMEISTAGSNLYOTGDHTAVVPTNAGAEVDRLQVFGKRGKESVINKK
	<i>A. ochraceus</i>	291	FWVKDRNCLHMEISTAGSNLYOTGDHTAVVPTNAGAEVDRLQVFGKRGKESVINKK
	<i>S. cerevisiae</i>	280	FWVKDRNCLHMEISTAGSNLYOTGDHTAVVPTNAGAEVDRLQVFGKRGKESVINKK
30	<i>A. niger</i>	350	HDVAKVPIPTPTTYDAAVRYLVKCAPVSROFVTLAAPFAIRKATQVQVYVQG--L
	<i>A. ochraceus</i>	351	HDVAKVPIPTPTTYDAAVRYLVKCAPVSROFVTLAAPFAIRKATQVQVYVQG--L
	<i>S. cerevisiae</i>	338	HDVAKVPIPTPTTYDAAVRYLVKCAPVSROFVTLAAPFAIRKATQVQVYVQG--L
35	<i>A. niger</i>	409	PRCHTQMLTAAQALQISIKKPFVAVPFSLLTGLTQAPRYVISSSSSVQDKTISL
	<i>A. ochraceus</i>	411	PRCHTQMLTAAQALQISIKKPFVAVPFSLLTGLTQAPRYVISSSSSVQDKTISL
	<i>S. cerevisiae</i>	398	PRCHTQMLTAAQALQISIKKPFVAVPFSLLTGLTQAPRYVISSSSSVQDKTISL
40	<i>A. niger</i>	468	AVVESVRLF--SASVKGCTVNNLALAKKQNRSSSR--SRLDHLHGGPRKYGDIHV
	<i>A. ochraceus</i>	470	AVVESVRLF--SASVKGCTVNNLALAKKQNRSSSR--SRLDHLHGGPRKYGDIHV
	<i>S. cerevisiae</i>	458	AVVESVRLF--SASVKGCTVNNLALAKKQNRSSSR--SRLDHLHGGPRKYGDIHV
45	<i>A. niger</i>	525	GVHVRHSNFKLPSPDSRPLVWGEGTGVAFFPGFIQERAAALAKGSR-----VGTNLE
	<i>A. ochraceus</i>	527	GVHVRHSNFKLPSPDSRPLVWGEGTGVAFFPGFIQERAAALAKGSR-----VGTNLE
	<i>S. cerevisiae</i>	518	GVHVRHSNFKLPSPDSRPLVWGEGTGVAFFPGFIQERAAALAKGSR-----VGTNLE
50	<i>A. niger</i>	579	EGCRKSDDEFLYKDFRKTQVQLGLNKLITAFSRE-GPKVYVQIRIRFSEGLVSDLL
	<i>A. ochraceus</i>	581	EGCRKSDDEFLYKDFRKTQVQLGLNKLITAFSRE-GPKVYVQIRIRFSEGLVSDLL
	<i>S. cerevisiae</i>	578	EGCRKSDDEFLYKDFRKTQVQLGLNKLITAFSRE-GPKVYVQIRIRFSEGLVSDLL
	<i>A. niger</i>	638	OKATFYVCGDAANMAREVNLVGLQIALVGLPAKKGEEVKKHRRRSRYQVDVWS
	<i>A. ochraceus</i>	640	OKATFYVCGDAANMAREVNLVGLQIALVGLPAKKGEEVKKHRRRSRYQVDVWS
	<i>S. cerevisiae</i>	637	OKATFYVCGDAANMAREVNLVGLQIALVGLPAKKGEEVKKHRRRSRYQVDVWS
	<i>A. ochraceus</i>	PMON45632	(SEQ ID NO: 05)
	<i>A. niger</i>		(SEQ ID NO: 38)
	<i>S. cerevisiae</i>	yeast	(SEQ ID NO: 37)

10021425-103004

Figure 9 – Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* and human oxidoreductase to reductases from *A. niger*, yeast, and mouse.

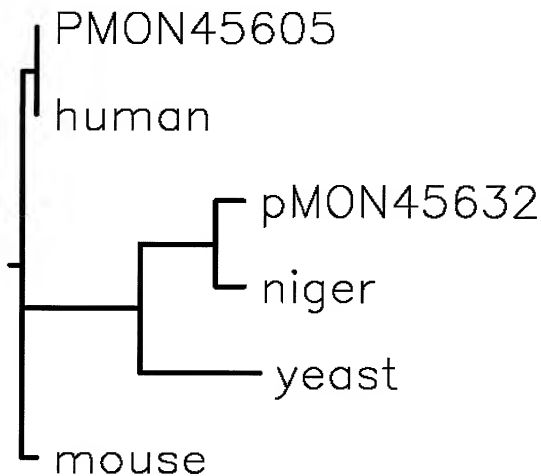


Figure 10 – Percent homology between *Aspergillus ochraceus* oxidoreductase to reductases from *A. niger*, yeast, and mouse and human.

Accession number	organism	% id to <i>A.och</i> oxred
CAA81550	<i>A. niger</i>	84
BAA02936	<i>S. cerevisiae</i>	37
BAA04496	mouse	34
AAB21814	human	33

10321425-103001

Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

5	PMON45605	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
	human	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
	rabbit	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
	rat	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
10	mouse	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
	pig	1	MGDSHVDTSTLSEAVAREVSLFSMTDMLFSLIVGLLTWIFPRKKKEVPEEIKTQTL
15	PMON45605	61	TSSVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
	human	61	TSSVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
	rabbit	61	TSSVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
	rat	61	APPVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
20	mouse	61	APPVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
	pig	61	TSSVFSSFEVRKKKTGRNTLVFYGSVGTABFPANRLSKDAHRYGMRGMSADPPEYD
25	PMON45605	120	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
	human	120	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
	rabbit	121	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
	rat	120	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
30	mouse	120	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
	pig	120	ADLSSLPETIDNALVVRCAATYGECDPTNAODFYDNLQEDVDLGVKFAVFGNGKTYE
35	PMON45605	180	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
	human	180	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
	rabbit	181	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
	rat	180	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
40	mouse	180	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
	pig	180	HFNANGKYVLRLEQLGAORTFELGLGDDGDNLEEDFTVIREQFWPAVCEHGVGEATGE
45	PMON45605	240	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
	human	240	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
	rabbit	241	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
	rat	240	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
50	mouse	240	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
	pig	240	SSIRQVELVWHTDLEAKVYGEGRGLKSYENQKPPFDANKNPLAAVITNRKLNQOTERH
55	PMON45605	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	human	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	rabbit	301	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	rat	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	mouse	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	pig	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOIGFLGADLVVMSINIDDESNKKH
	PMON45605	360	PFPCPTVNTALTYVYLDITNPPTINVLVELAQYASEPSEDELRKMASSSGEGKEKLYSN
	human	360	PFPCPTVNTALTYVYLDITNPPTINVLVELAQYASEPSEDELRKMASSSGEGKEKLYSN
	rabbit	361	PFPCPTVNTALTYVYLDITNPPTINVLVELAQYASEPSEDELRKMASSSGEGKEKLYSN
	rat	360	PFPCPTVNTALTYVYLDITNPPTINVLVELAQYASEPSEDELRKMASSSGEGKEKLYSN

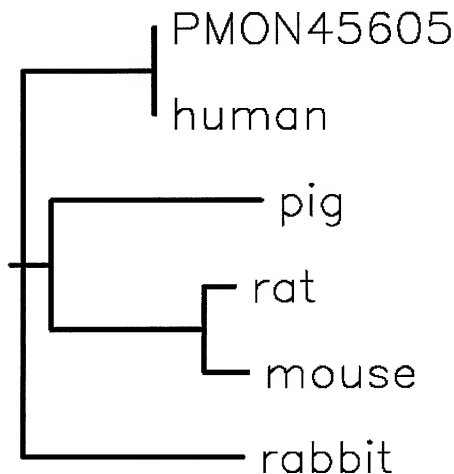
mouse	360	PFPCPTVPTALITYYLDIYNPPRTNVLVELAQYASEPSEDAIRKMASSSGGCKELYLSK
pig	360	PFPCPTVPTALITYYLDIYNPPRTNVLVELAQYASEPSEDAIRKMASSSGGCKELYLSK
5		
PMON45605	420	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
human	420	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
rabbit	421	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
rat	420	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
mouse	420	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
10		
pig	420	VVEARRHITALLQDPSLRPPIDHLCCLLPRLQARYYSTASSSKVHPNSVHICAVVWEYE
PMON45605	480	TKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI
human	480	TKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI
15		
rabbit	481	TKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI
rat	480	AKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI
mouse	480	AKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI
pig	480	TKSGRVNKGVAISWLRAKSPAGENGGRALVPMFVRKSOQRLPPKATTPVIVAGPGTGVAI

10301425-103001

5	PMON45605	540	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
	human	540	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
	rabbit	541	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
	rat	540	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
	mouse	540	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
	pig	540	PIGPIQERAWLRQCKGKEVGETLLYYGCRSDSDYLYREELAQPHDQALITQLNVAFSREQ	
10	PMON45605	600	EHKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
	human	600	EHKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
	rabbit	601	EHKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
	rat	600	EHKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
	mouse	600	EHKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
15	pig	600	PCVKVYVOHLLKRDSEHLWKLITHEGGAHIVCGDARNMARDVONCFYDILVABLEGEHQAQ	
20	PMON45605	659	VDYIKKILMTKGRYSLDWMS	(SEQ ID NO: 03)
	human	659	VDYIKKILMTKGRYSLDWMS	(SEQ ID NO: 52)
	rabbit	661	VYVKKILMTKGRYSLDWMS	(SEQ ID NO: 53)
	rat	660	VYVKKILMTKGRYSLDWMS	(SEQ ID NO: 54)
	mouse	660	VYVKKILMTKGRYSLDWMS	(SEQ ID NO: 55)
	pig	660	VYVKKILMTKGRYSLDWMS	(SEQ ID NO: 56)

10021425.103001

Figure 12 – Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt

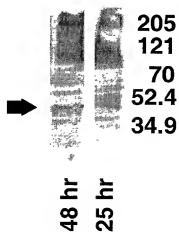


10345

10345

Figure 14 - Expression of *Aspergillus ochraceus* 11 α hydroxylase in transfected Sf9 insect cells

Expression of 11- α -Hydroxylase in Transfected Sf9 Cells



1002442001

Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

